

Purification Result for Endo- $\beta$ -N-acetylglucosaminidase (15-25% gradient SDS-PAGE)

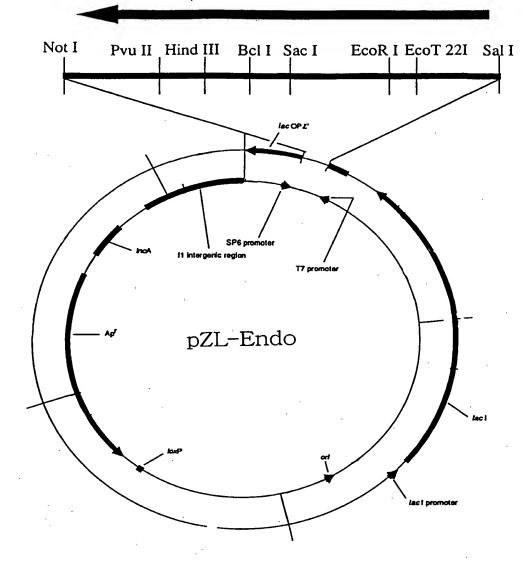
Lane 1: Purified endo-  $\beta$  -N-acetylglucosaminidase from *Mucor hiemalis* 

Lane 2: Molecular weight markers

FIG. 2



Novel endo- $\beta$  -N-acetylglucosaminidase gene



Restriction enzyme map for pZL-Endo including the full-length novel endo-  $\beta$  -N-acetylglucosaminidase gene.



10 GTCGACCCAC	20 20 20	30 ACGCGTCGGC	40 GGACGCGTGG	50 GCGGACGCGT	GGGTTTTATT
70 TTACATAAAT	08 ATGCCTTCAC	90 TTCAATTGCA	100 ACCTGATGAC	110 AAACTAGCAC	120 CIGITICITI
130 TOCACTTAAG	140 TCTATGAATG		160 CTGGACGCCA	170 GACGAAAAGA	180 TAAAGTTTAA
190 CGTTTCAAGC	200 GTGGCACTAC	210 AGCCTCGTGT	220 GAAAAACGCC	230 CTGAAACCTC	.240 AATTATTGTT
250 AACTCATGAT	260 ATGGCAGGAG	270 GATATAAAGA	280 AGATAAAAAT	290 ATTCAAGGAA	300 ACAATTATAA
310 AGACATTTAT	320 AAÇATTCAAT	330 ATTGGCATTT	340 AGCTGATACT	350 TITGTATATT	360 TCTCTCATGA
370 GCGAGTTAGC	380 ATTCCTCCAG	390 TCAATTGGAC	400 AAATGCTTGT	410 CATAGAAATG	420 GTGTAAAGTG
430 TTTAGGTACT	440 TTTTTAGTAG	450 AAGGAAATAA	460 CCAAATGCAT	470 GAAATGGAAG	480 CCTTGCTTCA
490 CGGTCCACCT	500 TTACTTAATA	510 ACACTGACGA	520 CCCTATGAGA	530 TTATGGAGTC	540 CGTATTATGC
550 AGACCAATTA	560 GTTGCTATTG	570 CTAAACACTA	580 TGGTTTTGAT	590 GGCTGGTTGT	600 TCAATATTGA
ATGCGAATIC	620 TTTCCTTTTC	630 CTACAAATCC	640 AAAATTCAAA	650 GCTGAAGAGT	660 TGGCAAAGTT
670 TCIACACIAT	TTTAAGGAAA	AATTGCATAA		GGATCTCAAC	TCATTTGGTA
	ACAAATGAAG	GAGAAATCCA		CAGCTCACAT	GGAAAAATGA
GITATITITT	800 AAAAACACGG	ATGGTATTTT	TTTGAATTAT	TGGTGGAAAA	AAGAATACCC
TGAAATGGCG	860 CGTAGAGTAG	CTGAAGGAAT	AGGTAGATCA	GGTTTAGAAG	TTTATTTTCG
TACAGATGTA	920 TGGGGAAGGC	ATACTTATGG	TGGCGGTGGT	TTCAAATCAT	ATAAGGGTGT
AAAAACIGCC		TGACATCTTC	TGCATTATTT	GGTATGGCAT	GGACATACGA
GCATTICGAA		TTGAAAAGAT	GGATCGTTTG	TTTTGGTGTG	GTGGTAAATA
CTCTGACTAT		CICCTAAAAA	CCCAGATGAC	GAAAAAGAAG	TAGAAAGCGA
TGATAGTGAA		TGTACGGACA	CAAGAAAGGT	ATTGCTGACA	CGGTAGAATC
1210 TATTCCTGTA	CCAGGAACAG	Attograter		GATAGGGGGT	TTGGAAATAG
GTTTTATTAT		GATTACTITC	TCAGCCTTGG	TCCCATTTAT	CGCATCAAGC
1330 TATTCTCCCC	1340 AATAAAAGCT	1350 ATCGAAATCC	1360 AGAGATTTAT	1370 CCCACTGATC	1380 AAAACATTAA

Entire nucleotide sequence of the fragment inserted into the Sal I-Not I sites of pZL-Endo including the full-length novel endo- $\beta$ -N-acetylglucosaminidase gene.



Г					
139	0 140 T TCTCTCGAT	0 141	0 142	0 1430	1440
AATCACTAG	T TCTCTCGAT	T GCGATCATO	G AGCTTTTCT	r GGTGGAACC	ע ביידים יידע ען דע ביידים יידע דע ען
145	146	0 147	0 1480	1490	1500
CAAAGGCCA	A CGTTTCAAT	C ATAGAGAATY	C GCATGATGT	GAAACTGAAA	TTAGTATACC
151	0 150	0 4 =	_		
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ICIGIAIAA	G CTTTCATTA	S ATGCTAGTA	A AGGATGCTCA	TTGCGTTATA	TTTAŢAGAAC
157	0 1580	1500	1.500		
TTTGTTGAT	G AAAGATGTA	ACTURACION A	1000	1610	1620
1630	1640	1650	1560	1670	
CTCAGTTAA:	TTCTTCAAGO	TATGGCAGCC	AGATGAAAAT	7010 P	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
1690	1700 A GCCACTGTT	1710	1720	1730	1740
TGGAATGAG	A GCCACTGTTA	CAACTGAAAA	TTCTACCGAA	AGCAGATGCT	ייייייייייייייייייייייייייייייייייייי
1/50	1760 A GAAGATACAC	1770	1780	1790	1800
THUMACHEAN	A GAAGATACAG	GAGAAAATGA	TTGGATAACA	AAAACTATTA	ATGTGCCTGC
1810	1920	1020			
TGTTCCAGA	1820 GGAACTCAAT	T830	1840	1850	1860
	GGAAGTCAAT	INIACATIAC	AAGACTIGAA	GIGAGCGTAG	TATTAGATAC
1870	1880	1990	1000		
AGCTGGTTTA	GIAGGICTIG	TTAATCAAGT	TATTICCTITICC	TATO	1920
1930	1940	1950	1960	1970	1990
ACCAACTATA	AATTCTGGAA	TAAAAACAGA	TTCATCACGC	ATTATTCAGG	ATCTCTTTTG
1000					
CAAACAMCAC	2000	2010	2020	2030	2040
GUNNOWI CHO	AAATATACCA	AAATCGGAAA	AGAAAGTTTA	GACGACATAG	CTCAAGAAGA
2050	2060	2070	2222		
AGTTCATAGA	TATTATOGAA	Catrica actro	2080	2090	2100
		CHICANCIG	GGAAAACACA	GCAAATGTAG	TAAACGCTTG
. 2110	2120 GATTACTACA	2130	2140	2150	21.00
<b>GGAGGAAATA</b>	GATTACTACA	ACGTTTTTTA	CAAAGAAAGT	GACGACTCTG	CDDCTCCDT
2170	2180	2190	2200	2210	2220
CTTTTTAGGA	ACAGCATTCT	GTAATCAATT	TCGTGTATCT	GGTTTAGATA	TTATTTTATC
2230	2240				
ACCEPTED ART	A ACATTACTURA	2250	2260	2270	2280
		TIGHNOCIGI	TAACAAAGAA	GGATACATCT (	CTTCAAGTGG
2290	2300	2310	2220	0070	
TAGCATAGAT	TIGICATTAA	ACTAGGACTT	עבכב המממת GAAATA	עראגייייינער אייייינער איייייינער אייייייינער אייייייינער אייייייינער איייייינער איייייינער איייייינער איייייי	2340
				niimiGATAA A	<b>АДААААА</b> А
2350	2360 <b>AAAAAAAA</b> G	2370	2380	2390	2400
AAAAAAAA	AAAAAAAAAG	GGCGGCCGC.	• • • • • • • • • •		2400
					<b></b>

Entire nucleotide sequence of the fragment inserted into the Sal I-Not I sites of pZL-Endo including the full-length novel endo- $\beta$ -N-acetylglucosaminidase gene. (Continued)

FIG. 5



		9	)		18			27	,		3	5		49			54
ATC	cc1	TCA		CAA			cci	GAT	GAC	CAA	A CT	A GCA	CCI	GM	TCI	וייד י	CCA
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CTI	AAC	63 TCT		AAT	72 GAG		AGG	81 GAC	TOC	ACC	90 CC2	) A GAC	GAA	99 . AAG	ATA	AAG	108
L	ĸ	s	M	N	E	L	R	D	W	т	P	D	E	к	I	ĸ	F
AAC	GTT	117 TCA	AGC	GIG	126 GCA	CTA	CAG	135 CCT		GIG	144 AAA	AAC	GCC	153 CTG	AAA	ccr	162 CAA
N	V	s	s	v	A	L	Q	P	R	v	K	N	A	L	к	P	Q
TTA	TIG	171 TTA	ACT	CAT	180 GAT	ATG	GCA	189 GGA		TAT	198 ' AAA	GAA	GAT	207 AAA	AAT	ATT	216 CAA
L	L	L	T	н	D	м	A	G	G	Y	K	E	D	K	N	ī	 Q
GGA	AAC	225 AAT	TAT	AAA	234 GAC	ATT	TAT	243 AAC	ATT	CAA	252 TAT	TGG	CAT	261 TTA	GCT	GAT	270 ACT
G	N	N	Y	K	D	I	Y	N	Ţ	Q	Y	W	Н	L	A	ם	T
TTT	GTA	279 TAT	TTC	TCT	288 CAT	GAG	CGA	297 GTT	AGC	ATT	306 CCT	CCA	GTC	315 AAT	TGG	ACA	324 AAT
F	v	Y	F	s	H	E	R	V,	S	1	P	P	v	N	W	T	N
GCT	TGT	333 CAT	AGA	AAT	342 GGT	GTA	AAG	351 TGT	TTA	GGT	360 ACT	TTT	TTA	369 GIA	GAA	GGA	378 AAT
A	С	H	R	N	G	V	K	С	L	G	T	F	L	v	E	G	N
AAC	CAA	387 ATG	CAT	GAA	396 · ATG		GCC	405 TTG	CTT	CAC	414 GGT	CCA	CCT	423 TTA	CIT	AAT	432 AAC
N	Q	M	H	E	M	E	A	L	L	H	G	·P	P	L	L	N	N
ACT	GAC	441 GAC	сст 		450 AGA	TTA		459 AGT	CCG	TAT	468 TAT	GCA	GAC	477 CAA	TTA	GTT	486 GCT
T	D	D	P	M	R	L	W	S	P	Y	Y	A	D	Q	L	v	A
ATT	GCT	495 AAA	CAC		504 GGT	TTT 	GAT	513 GGC	TGG	TIG	522 TTC	AAT		531 GAA	TGC	GAA	540 TTC
I	A		H				D	G	W	L	F	N	I	E	С	E	F
		549 TTT		ACA		CCA	AAA					GAG					~
F	P	F	P	T	N	P	K	F	K	A	E	E	L	A	K	F	L
CAC	TAT	603 TTT	AAG		612 AAA	TTG	CAT	621 AAC	GAA	ATA	630 CCT	GGA	TCT	639 CAA	CIC	ATT	648 TGG
Н	Y	F	K	E	K	L	Н	N	E	I	P	G	s	Q	L	I	W
		657 AGC .		ACA	AAT (		GGA (	GAA		CAC			AAC			ACA	702 TGG
Y	D	S	M.	T	N	E	G	E	I	H	W	Q	N	Q	L	T	W

Amino acid sequence deduced from the novel Endo- $\beta$ -N-acetylglucosaminidase gene, and the nucleotide sequence of the DNA encoding this amino acid sequence.

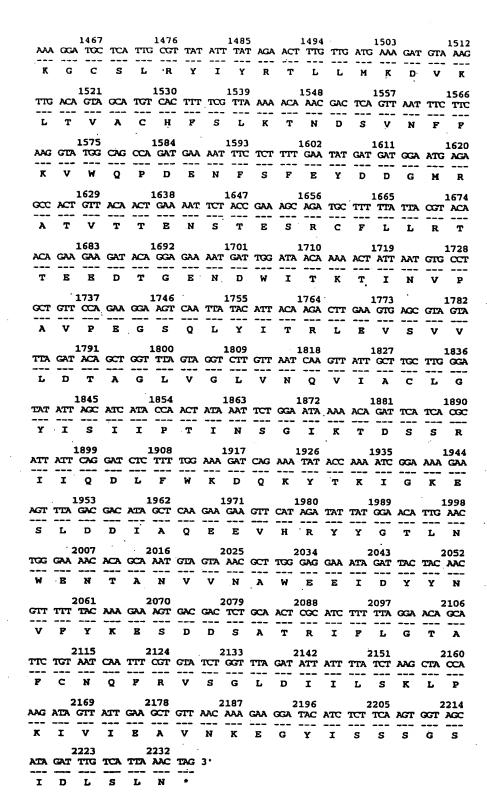
FIG. 6



		711			720			729			738			747			756
AAA	AAT	GAG	TTA	TTT	TTT	AAA	AAC	ACG	GAT	CCT	ATT	TTT	TTG	AAT	TAT	TCG	TCC
ĸ	N	E	L	F	F	к	N	т	D	G	I	F	L	N	Y	W	W
AAA	AAA	765 GAA	TAC	CCT	774 GAA	ATG	GCG	783 CGT	AGA	GTA	792 GCT	GAA	GGA	801 ATA	CCT	AGA	810 TCA
				 P				 R	R	v		 E		I		 R	
K	•	819	*	F	828	M	^	837	K	•	846		J	855	Ğ	K	864
GGT	TTA	GAA	GTT	TAT		GCT	ACA		GTA	TGG		AGG	CAT		TAT	GGT	
G	L	E	V	Y	F	G	T	D	V	W	G	R	Н	T	Y	G	G
GGT	GGT	873 TTC	AAA	TCA	882 TAT	AAG	GGT	891 GTA	AAA	ACT	900 GCC	TAC	TCT	909 GCA	ATG	ACA	918 TCT
G	G	F	K	S	Y	ĸ	G	V	K	T	. <b>A</b>	Y	S	A	M	T	. <b>S</b>
		927	_		936			945		<b></b>	954		<b>~</b>	963			972
TCT	GCA	TTA	TTT	GGT	AIG	GCA	TGG	ACA	TAC	GAG	CAT	TIC	GAA	AAG	TCT	GAA	TTT
s	A	Ĺ	F	G	M	A	W	T	Y	E	H	F	E	K	s	E	F
		981			990			999		:	L008		:	1017		;	1026
GAA	AAG	ATG	GAT	CGT	TTG	TTT	TGG	TGT	CCT	CCT	AAA	TAC	TCT	GAC	TAT	ccr	ccc
E	ĸ	M	D .	R	τ.	F	w	c	G	G	ĸ	Y	s	D	Y	P	P
_			_			-		_	_			_	_		_	_	_
CCA		1035 CCT	AAA		CCA	GAT		1053 GAA		GAA		GAA		1071 GAT	GAT		1080 GAA
P	P	P	ĸ	N	P	. В	ט	E	K	E	V	E	S	D	D	s	E
		1089			1098			1107			1116			1125			1134
GAT		CTC	ATG			CAC			GGT			GAC			GAA		
GAT  D	GAG		ATG M		GGA.	CAC H	AAG				GCT			GIA	GAA  E	TCT	
	GAG E	CTC		TAC Y	GGA.		AAG K	AAA		ATT I	GCT		ACG T	GIA		TCT	ATT
D	GAG E	CTC L	M	TAC Y	GGA G L152	н	AAG K	AAA K 1161	G	ATT I	GCT A	D	ACG T	GTA V L179	 E	TCT	ATT I
D	GAG E	L L L L143 CCA	M	TAC Y	GGA G 152 GAT	H TGG	AAG K	K 161 GTT	G ACC	ATT I AAT	GCT A	D GAT	ACG T	V V L179 GGG	 E	TCT S	ATT I
D CCT	GEAG E GEA	L L L143 CCA P	M	TAC Y ACA	GGA G L152 GAT D	H TGG	AAG K TTT	K 161 GTT V	G ACC	ATT I AAT N	GCT A 1170 TTT F	D GAT	ACG T AGG R	V 179 GGG  G	E	TCT S GGA G	ATT I 1188 AAT N
D CCT P	GAG E GTA V	L L L L143 CCA	M GGA G	Y ACA T	GGA G 1152 GAT D	H TGG W	AAG K TIT F	K 1161 GTT V	G ACC T	ATT	GCT A 1170 TTT F	D GAT D	ACG T AGG R	V 1179 GGG  G	TTT  F	TCT S GGA G	I 1 1188 AAT N L242
D CCT P	GAG E GTA V	L L L143 CCA P L197 TAT	M GGA G	TAC Y ACA T	GGA G 1152 GAT D 206 GGA	H TGG W	AAG	AAA K 1161 GTT V 215 TTA	G ACC T	AAT N	A 1170 TIT F	D GAT D CCT	ACG T AGG R TGG	V L179 GGG G L233 TCC	E TTT F	TCT S GGA G TTA	I I I I I I I I I I I I I I I I I I I
D CCT P	GAG E GTA V TTT	CTC L L143 CCA P L197 TAT Y	M GGA G	Y ACA T AGA R	GGA G I152 GAT D I206 GGA GGA	H TGG W	AAG K TTT F AGA R	AAA K 1161 GIT V 1215 TTA L	G ACC T	AAT AAT N TCT	GCT A 1170 TIT F 1224 CAG Q	D GAT D CCT	ACG T AGG R TGG	V L179 GGG  G L233 TCC	TTT  F	GGA G TTA	III88 AAT N L242 TCG S
D CCT P	GAG E GTA V TTT	L L L143 CCA P L197 TAT	M GGA G TAT	Y ACA T AGA R	GGA G 1152 GAT D 206 GGA GGA	TGG W AAG	AAG TTT F AGA R	AAA  K 1161 GIT  V 1215 TTA  L	G ACC T	AAT I AAT N TCT	GCT A 1170 TTT F 1224 CAG Q	D GAT D CCT	ACG T AGG R TGG	GTA V L179 GGG  G L233 TCC  S	E TTT F CAT	S GGA G TTA	III88 AAT N L242 TCG S L296
D CCT P	GAG E GTA V TTT	L L L L L L L L L L L L L L L L L L L	M GGA G TAT Y ATT	Y ACA T AGA R CTC	GGA 	H TGG W AAG K AAT	AAG TTT F AGA R	K 161 GTT V 215 TTA L 269 AGC	G ACC T	ATT I AAT N TCT S CGA	GCT A 170 TTT F 224 CAG Q 1278 AAT	D GAT D CCT P	ACG T AGG R TGG W GAG	V 1179 GGG G 1233 TCC  S	E TTT F CAT H TAT	GGA TTA L	I 188 AAT N L242 TCG S L296 ACT
D CCT P	GAG E GTA V TTT	L L L L L L L L L L L L L L L L L L L	M GGA G TAT	Y ACA T AGA R	GGA G 1152 GAT D 206 GGA GGA	TGG W AAG	AAG TTT F AGA R	AAA  K 1161 GIT  V 1215 TTA  L	G ACC T	AAT I AAT N TCT	GCT A 1170 TTT F 1224 CAG Q	D GAT D CCT	ACG T AGG R TGG	GTA V L179 GGG  G L233 TCC  S	E TTT F CAT	S GGA G TTA	III88 AAT N L242 TCG S L296
D CCT P AGG R CAT	GAG E GTA V TTT F CAA	L143 CCA P L197 TAT Y L251 GCT A	M GGA G TAT Y ATT	TAC Y  ACA T  AGA R  CTC	GGA G 152 GAT D 206 GGA GGA CCC P P 1314	TGG W AAG K AAT	AAG F AGA R AAA	AAA K 161 GTT V 1215 TTA L 1269 AGC S 1323	G ACC T	AAT AAT N TOT S CGA R	GCT A 1170 TTT F 1224 CAG Q 1278 AAT N 1332	D GAT D CCT P	ACG T AGG R TGG W GAG	GTA V 1179 GGG G 1233 TCC S 1287 ATT I	E TTT F CAT H TAT	GCA GCC TTA L CCC	ATT I 1188 AAT N L242 TCG S L296 ACT T
D CCT P AGG R CAT	GAG E GTA V TTT F CAA	L L L L L L L L L L L L L L L L L L L	M GGA G TAT Y ATT	TAC Y  ACA T  AGA R  CTC	GGA G 152 GAT D 206 GGA GGA CCC P P 1314	TGG W AAG K AAT	AAG F AGA R AAA	AAA K 161 GTT V 1215 TTA L 1269 AGC S 1323	G ACC T	AAT AAT N TOT S CGA R	GCT A 1170 TTT F 1224 CAG Q 1278 AAT N 1332	D GAT D CCT P	ACG T AGG R TGG W GAG	GTA V 1179 GGG G 1233 TCC S 1287 ATT I	E TTT F CAT H TAT	GCA GCC TTA L CCC	ATT I 1188 AAT N L242 TCG S L296 ACT T
D CCT P AGG R CAT H	GAG E GTA V TTT F CAA	L143 CCA P L197 TAT Y L251 GCT A	M GGA G TAT Y ATT I	TAC Y ACA T AGA R CTC L AAA	GGA G 1152 GAT D 206 GGA G 1260 CCC P 1314 ATC	TGG W AAG K AAT N ACT	AAG  TTTT  F  AGA  R  AAAA  K  AGT	AAA K 1161 GTT V 2155 TTTA L 1269 AGC S 1323	G ACC T T CTT L TAT Y	ATT I AAT N TCT CGA R GAT	GCT A	GAT D CCT P CCA P	ACG T ACG R TGG W GAG CAT	GTA V 1179 GGG G G 1233 TCC S 1287 ATT I 1341 GGA	E TTT F CAT H TAT Y	S GGA TITA L CCCC	ATT I 1188 AAT N 1242 TCG S 1296 ACT T 1350 CTT
D CCT P AGG R CAT H GAT	GAG  GTA  V  TTT  F  CAA  Q  CAA	CTC	M GGA G TATT Y ATT I	TAC Y ACA T AGA R CCTC L AAAA K	GGA G 1152 GAT D 1206 GGA G 1260 CCC P 1314 ATC I 1368	H TGG W AAG K AAT N ACT	AAG TTTT F AGA AAA AAA K AGT S	AAA 	G ACC TT TAT TAT Y.	ATT I AAT N 1 TCT S CGA R GAT D	GCT A 1170 TTT F 1224 CAG Q 1278 AAT N 1332 TGC C 1386	D GAT P GAT D	ACG T AGG R TGG W GAG CAT H	GTA V 1179 GGG G 1233 TCC S 1287 ATT I 1341 GGA G 1395	E TITT F CAT H TAT Y GCT A	GGA G TTTA L CCCC P	ATT I 1188 AAT N 1242 TCG S 1296 ACT T 1350 CTT L 1404
D CCT P AGG R CAT H GAT	GAG  GTA  V  TTT  F  CAA  Q  CAA	L L L L L L L L L L L L L L L L L L L	M GGA G TATT Y ATT I	TACA Y ACA T AGA R CTC L AAAA K CTT	GGA G 1152 GAT D 1206 GGA G 1260 CCC P 1314 ATC I 1368	TGG W AAG K AAT N ACT T	AAG TTTT F AGA R AAA K AGT S	AAA K 1161 GIT V 1215 TTA L 1269 AGC S 1323 TCT S 1377 GGC	G ACC TT TAT TAT Y.	ATT I AAT N TCT S CGA R GAT D	GCT A 1170 TTT F 1224 CAG Q 1278 AAT N 1332 TGC C 1386	D GAT P GAT D	ACG T AGG R TGG W GAG CAT H	GTA V 1179 GGG G 1233 TCC S 1287 ATT I 1341 GGA G 1395	E TITT F CAT H TAT Y GCT A	GGA G TTTA L CCCC P	ATT I 1188 AAT N 1242 TCG S 1296 ACT T 1350 CTT L 1404
D CCT P AGG R CAT H GAT D	GAG  GTA  V  TTTT  F  CAA  Q  CAA  Q  GGA	CTC	M GGA G TAT Y ATT I TCG	TAC Y ACA T AGA R CTC L AAAA K CTT	GGA	H TGG W AAG K AAT N ACT T	AAG  TTTT  F  AGA  AAA  K  AGT  AAAA	AAA  K ill61 GIT  V ill62 TTA  L ill63 TTA  L ill63 TTA  S ill63 TTA  S ill77 GGC  S ill77	G ACC T CTT L CTC L CAA	ATT I AAT N TCT S CGA R GAT D	GCT	D GAT D CCT P CCA P GAT D	ACG T ACG R TGG GAG CAT H CAT	GTA V 1179 GGG G 1233 TCC S 1287 ATT I 1341 GGA G 1395 AGA	E TITT F CAT H TAT Y GCT A	GGA G TTTA L CCCC P TTTT F	1188 AAT N L242 TCG T 1350 CTT L
D CCT P AGG R CAT H GAT D	GAG  GTA  V  TTT  F  CAA  Q  CAA  GGA  GGA	CTC	M GGA G TAT Y ATT I TCG	TAC Y ACA T AGA R CCCC L AAAA K CTT L	GGA	H TGG W AAG K AAT N ACT T	AAGA R AAAA K AGT S AAAA K	AAA K 1161 GTT V 1215 TTA L 1269 AGC S 1323 TCT S 1377 GGC G	G ACC T CTT L CTC L CAA	ATT I AAT N TCT S CGA R GAT D CGT R	GCT A 1170 TTT F 1224 CAG Q 1278 AAT N 1332 TGC C 1386 TTC F	D GAT D CCT P CCA P GAT D	ACG T AGG R TGG W GAG CAT H CAT H	GTA V 1179 GGG G 1233 TCC S 1287 ATT I 1341 GGA G 1395 AGA	E TTT F CAT H TAT Y GCT A GAA E	GGA G TTTA L CCCC P TTTT F	ATT I 1188 AAT N 1242 TCG T 1350 CTT L 1404 CAT H
D CCT P AGG R CAT H GAT D	GAG  GTA  V  TITT  F  CAA  Q  CAA  GGA  GGA	L 1143 CCA P 1197 TAT Y 1251 AACC N 1359 ACC	M GGA G TAT Y ATT I TCG S	TAC Y ACA T AGA R CCTC L AAAA K CTT L AAAA	GGA G 1152 GAT D 1206 GGA G 1260 CCC P 1314 ATC I 1368 ATT I 1422	H TGG W AAG K AAT N ACT T	AAGA R AAAA K AAAA K	AAA K 1161 GIT V 1215 TTA L 1269 AGC S 1323 TCT S 1377 GGC G G	G ACC T T TAT Y CTC L CAA Q	ATT I AAT N TCT S CGA R GAT D CGT	GCT A 1170 TTT F 1224 CAG Q 1278 AAT N 1332 TGC C 1386 TTC F 1440	D GAT P GAT D	ACG T AGG R TGG W GAG CAT H	GTA	E TITT F CAT H TAT Y GCT A GAA E	GGA G G TTTA L CCC P TTTT F	ATT I 1188 AAT N 1242 TCG T 1350 CTT L 1404 CAT H 1458

Amino acid sequence deduced from the novel Endo- $\beta$ -N-acetylglucosaminidase gene, and the nucleotide sequence of the DNA encoding this amino acid sequence. (Continued)

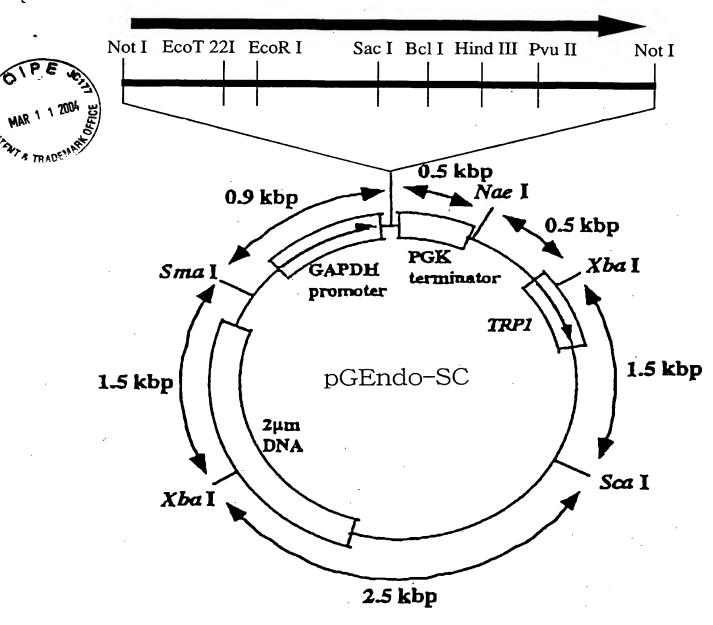




Amino acid sequence deduced from the novel Endo- $\beta$ -N-acetylglucosaminidase gene, and the nucleotide sequence of the DNA encoding this amino acid sequence. (Continued)

FIG. 8

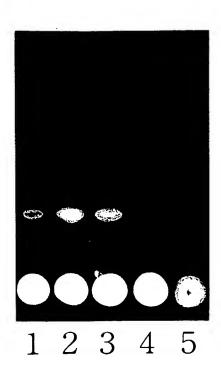
Novel endo- $\beta$ -N-acetylglucosaminidase gene



Structure of expression vector pGEndo-SC for the use in *Saccharomyces cerevisiae*, which comprises a novel endo- $\beta$ -N-acetylglucosaminidase gene.

FIG. 9





Expression of endo-  $\beta$  -N-acetylglucosaminidase enzyme in yeast into which an endo-  $\beta$  -N-acetylglucosaminidase gene has been introduced.

Lanes 1-3: Cellular extract of S. cerevisiae YPH500 (pep4) into which an endo- $\beta$ -N-acetylglucosaminidase gene has been introduced.

Lane 4: Purified endo- $\beta$ -N-acetylglucosaminidase derived from M. hiemalis

Lane 5: Cellular extract of S. cerevisiae YPH500 (pep4)